

SEQUENCE LISTING

<110> Holloway, James L.
Lok, Si

<120> SECRETED PROTEIN ZACRP4

<130> 99-29

<150> 60/141,928
<151> 1999-07-01

<160> 9

<170> FastSEQ for Windows Version 3.0

<210> 1

<211> 1357

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (210)...(1196)

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ctgcagcctg	cagccccgag	cccgccagccc	ggagccagat	cgccggctca	gaccgaaccc	180
gactcgaccg	ccgccccccag	ccagggcgc	atg ctg ccg	ctt ctg ctg	ggc ctg	233
			Met Leu Pro	Leu Leu Leu	Gly Leu	
			1	5		

ctg ggc cca	gctg	gcc tgc	tgg	gcc ctg	ggc ccg	acc ccc	ggc ccg gga	281
Leu Gly Pro	Ala	Ala Cys	Trp	Ala Leu	Gly Pro	Thr Pro	Gly Pro Gly	
10	15	20						

tcc tct gag	ctg	cgc tcg	gcc ttc	tcg	gct	gca	cgc acc acc	ccc ctg	329
Ser Ser Glu	Leu	Arg Ser	Ala Phe	Ser	Ala	Ala Arg	Thr Thr	Pro Leu	
25	30	35							

gag ggc acg	tcg	gag atg	gct	acc ttc	gac aag	gtg tac	gtg aac	377
Glu Gly Thr	Ser	Glu Met	Ala Val	Thr Phe	Asp Lys	Val Tyr	Val Asn	

45

50

55

atc ggg ggc gac ttc gat gtg gcc acc ggc cag ttt cgc tgc cgc gtg 425
 Ile Gly Gly Asp Phe Asp Val Ala Thr Gly Gln Phe Arg Cys Arg Val
 60 65 70

ccc ggc gcc tac ttc ttc tcc acg gct ggc aag gcc ccg cac aag 473
 Pro Gly Ala Tyr Phe Phe Ser Phe Thr Ala Gly Lys Ala Pro His Lys
 75 80 85

agc ctg tcg gtg atg ctg gtg cga aac cgc gac gag gtg cag gcg ctg 521
 Ser Leu Ser Val Met Leu Val Arg Asn Arg Asp Glu Val Gln Ala Leu
 90 95 100

gcc ttc gac gag cag cgg cgg cca ggc gcg cgg cgc gca gcc agc cag 569
 Ala Phe Asp Glu Gln Arg Arg Pro Gly Ala Arg Arg Ala Ala Ser Gln
 105 110 115 120

agc gcc atg ctg cag ctc gac tac ggc gac aca gtg tgg ctg ccg ctg 617
 Ser Ala Met Leu Gln Leu Asp Tyr Gly Asp Thr Val Trp Leu Arg Leu
 125 130 135

cat ggc gcc ccg cac tac gcg cta ggc gcg ccc ggc gcc acc ttc agc 665
 His Gly Ala Pro His Tyr Ala Leu Gly Ala Pro Gly Ala Thr Phe Ser
 140 145 150

ggc tac cta gtc tac gcc gac gct gac gcg cct gcg cgc ggg 713
 Gly Tyr Leu Val Tyr Ala Asp Ala Asp Ala Pro Ala Arg Gly
 155 160 165

ccg ccc gcg ccc ccc gag ccg cgc tcg gcc ttc tcg gcg gcg cgc acg 761
 Pro Pro Ala Pro Pro Glu Pro Arg Ser Ala Phe Ser Ala Ala Arg Thr
 170 175 180

cgc agc ttg gtg ggc tcg gac gct ggc ccc ggg ccg ccg cac caa cca 809
 Arg Ser Leu Val Gly Ser Asp Ala Gly Pro Gly Pro Arg His Gln Pro
 185 190 195 200

ctc gcc ttc gac acc gag ttc gtc aac att ggc ggc gac ttc gac gcg 857
 Leu Ala Phe Asp Thr Glu Phe Val Asn Ile Gly Gly Asp Phe Asp Ala
 205 210 215

gcg gcc ggc gtg ttc cgc tgc cgt ctg ccc ggc gcc tac ttc ttc tcc 905
 Ala Ala Gly Val Phe Arg Cys Arg Leu Pro Gly Ala Tyr Phe Phe Ser
 220 225 230

ttc acg ctg ggc aag ctg ccg cgt aag acg ctg tcg gtt aag ctg atg		953	
Phe Thr Leu Gly Lys Leu Pro Arg Lys Thr Leu Ser Val Lys Leu Met			
235	240	245	
aag aac cgc gac gag gtg cag gcc atg att tac gac gac ggc gcg tcg		1001	
Lys Asn Arg Asp Glu Val Gln Ala Met Ile Tyr Asp Asp Gly Ala Ser			
250	255	260	
cgg cgc cgc gag atg cag agc cag agc gtg atg ctg gcc ctg cgg cgc		1049	
Arg Arg Arg Glu Met Gln Ser Gln Ser Val Met Leu Ala Leu Arg Arg			
265	270	275	280
ggc gac gcc gtc tgg ctg ctc agc cac gac cac gac ggc tac ggc gcc		1097	
Gly Asp Ala Val Trp Leu Leu Ser His Asp His Asp Gly Tyr Gly Ala			
285	290	295	
tac agc aac cac ggc aag tac atc acc ttc tcc ggc ttc ctg gtg tac		1145	
Tyr Ser Asn His Gly Lys Tyr Ile Thr Phe Ser Gly Phe Leu Val Tyr			
300	305	310	
ccc gac ctc gcc ccc gcc ccg ccg ggc ctc ggg gcc tcg gag cta		1193	
Pro Asp Leu Ala Pro Ala Ala Pro Pro Gly Leu Gly Ala Ser Glu Leu			
315	320	325	
ctg tgagccccgg gccagagaag agcccgaggag ggccaggggc gtgcatgcca		1246	
Leu			
ggccggggccc gaggctcgaa agtcccgcgc gagcgcacg gcctccgggc ggcctggac		1306	
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<212> PRT			
<213> Homo sapiens			
<400> 2			
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Leu Gly Pro Thr Pro Gly Pro Gly Ser Ser Glu Leu Arg Ser Ala Phe			
20 25 30			
Ser Ala Ala Arg Thr Thr Pro Leu Glu Gly Thr Ser Glu Met Ala Val			
35 40 45			
Thr Phe Asp Lys Val Tyr Val Asn Ile Gly Gly Asp Phe Asp Val Ala			
50 55 60			

Thr Gly Gln Phe Arg Cys Arg Val Pro Gly Ala Tyr Phe Phe Ser Phe
 65 70 75 80
 Thr Ala Gly Lys Ala Pro His Lys Ser Leu Ser Val Met Leu Val Arg
 85 90 95
 Asn Arg Asp Glu Val Gln Ala Leu Ala Phe Asp Glu Gln Arg Arg Pro
 100 105 110
 Gly Ala Arg Arg Ala Ala Ser Gln Ser Ala Met Leu Gln Leu Asp Tyr
 115 120 125
 Gly Asp Thr Val Trp Leu Arg Leu His Gly Ala Pro His Tyr Ala Leu
 130 135 140
 Gly Ala Pro Gly Ala Thr Phe Ser Gly Tyr Leu Val Tyr Ala Asp Ala
 145 150 155 160
 Asp Ala Asp Ala Pro Ala Arg Gly Pro Pro Ala Pro Pro Glu Pro Arg
 165 170 175
 Ser Ala Phe Ser Ala Ala Arg Thr Arg Ser Leu Val Gly Ser Asp Ala
 180 185 190
 Gly Pro Gly Pro Arg His Gln Pro Leu Ala Phe Asp Thr Glu Phe Val
 195 200 205
 Asn Ile Gly Gly Asp Phe Asp Ala Ala Ala Gly Val Phe Arg Cys Arg
 210 215 220
 Leu Pro Gly Ala Tyr Phe Phe Ser Phe Thr Leu Gly Lys Leu Pro Arg
 225 230 235 240
 Lys Thr Leu Ser Val Lys Leu Met Lys Asn Arg Asp Glu Val Gln Ala
 245 250 255
 Met Ile Tyr Asp Asp Gly Ala Ser Arg Arg Arg Glu Met Gln Ser Gln
 260 265 270
 Ser Val Met Leu Ala Leu Arg Arg Gly Asp Ala Val Trp Leu Leu Ser
 275 280 285
 His Asp His Asp Gly Tyr Gly Ala Tyr Ser Asn His Gly Lys Tyr Ile
 290 295 300
 Thr Phe Ser Gly Phe Leu Val Tyr Pro Asp Leu Ala Pro Ala Ala Pro
 305 310 315 320
 Pro Gly Leu Gly Ala Ser Glu Leu Leu
 325

<210> 3

<211> 31

<212> PRT

<213> Artificial Sequence

<220>

<223> C1q Aromatic Motif

<221> VARIANT

<222> (2)...(6)

<223> Each Xaa is independently any amino acid residue

<221> VARIANT

<222> (7)...(7)

<223> Xaa is asparagine or aspartic acid

<221> VARIANT

<222> (8)...(11)

<223> Each Xaa is independently any amino acid residue

<221> VARIANT

<222> (12)...(12)

<223> Xaa is phenylalanine, tyrosine, tryptophan or
leucine

<221> VARIANT

<222> (13)...(18)

<223> Each Xaa is independently any amino acid residue

<221> VARIANT

<222> (20)...(24)

<223> Each Xaa is independently any amino acid residue

<221> VARIANT

<222> (26)...(26)

<223> Xaa is any amino acid residue

<221> VARIANT

<222> (28)...(28)

<223> Xaa is any amino acid residue

<221> VARIANT

<222> (30)...(30)

<223> Xaa is any amino acid residue

<221> VARIANT

<222> (31)...(31)

<223> Xaa is phenylalanine or tyrosine

<400> 3

Phe Xaa Xaa

1

5

10

15

Xaa Xaa Phe Xaa Xaa Xaa Xaa Gly Xaa Tyr Xaa Phe Xaa Xaa

20

25

30

<210> 4
 <211> 987
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Degenerate nucleotide sequence encoding the polypeptide of SEQ ID NO:2

<221> variation
 <222> (1)...(987)
 <223> Each N is A, T, G or C

<400> 4

atgytnccny tnytnytngg nytnytngn ccngcngcnt gytggcnyt nggnccnacn	60
ccnggnccnng gnwsnwsnga rytnmgnwsn gcnttysnng cngcnmgnac nacnccnytn	120
garggnacnw sngaratggc ngtnacnnyt gayaargtnt aygtnaayat hggngngay	180
ttygaygtng cnacnggnca rttymgntgy mngtnccnng gngcntaytt yttysnnty	240
acngcngnna argcncnca yaarwsnytn wsngtnatgy tngtnmgnaa ymgngaygar	300
gtncargcny tngcnttyga ygarcarmgm mgnccngng cnmgnmgnng ngnwsncar	360
wsngcnatgy tncarytna ytagggngay acngtntggy tnmgnynca yggngcnccn	420
caytaygcny tngngcncc ngnccnacn ttywsngnt ayytngtna ygcngaygc	480
gaygcngay cnccngcnmg ngnccnccn gcncnccnng arccnmgmws ngnnttysn	540
gcngcnmgnna cnmgnwsnyt ntnggnwsn gaygcngngc cnggnccnmg ncaycarccn	600
ytngcnttyg ayacngartt ygttnaayath gngngngayt tygngcngc ngnngngtn	660
ttymgntgym gnytnccnng ngnnttysn tnytngtna ygttnaayath gngngngayt	720
ttymgntgym gnytnccnng ngnnttysn tnytngtna ygttnaayath gngngngayt	780
aaracnytnw sngtnaaryt natgaraay mngngaygarg tncargnat gathtaygay	840
gayggngcnw smgnmgnmg ngaratgcar wsncarwsng tnatgytngc nytnmgnmgn	900
ggngngcng tntggtynt nwsncaygay caygagggnt ayggngcnda ywsnaaycay	960
ggnnaartaya thacnttysn gngnttysn gtntayccnng ayytngcncc ngnccnccn	987
ccnggnnytng gngcnwsnga rytnyt	

<210> 5
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Oligonucleotide ZC20,839

<400> 5

atgtacttgc cgtggttgct gtag

<210> 6

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Oligonucleotide ZC20840

<400> 6

cgacaccgag ttctgtcaaca ttg

23

<210> 7

<211> 325

<212> DNA

<213> Artificial Sequence

<220>

<223> Degenerate nucleotide sequence encoding the polypeptide of SEQ ID NO:2.

<221> variation

<222> (1)...(325)

<223> Each N is independently A, T, C or G.

<400> 7

ctggcccccgg	60
gcccggcac	120
caaccactcg	180
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cgagttcgtc	300
aacattggcg	325
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cgcggcgcc	
ggcgtgttcc	
gctgccgtct	
gnccggcgcc	
tacttcttct	
ncttcacgtct	
gggcaagctg	
ccgcgttaaga	
cgctgtcggt	
taagctgtatg	
aagaaccgcg	
acgaggtgca	
ggccatgatt	
tacgacgacg	
ggcgtcgcg	
gcgcggcgag	
atgcagagcc	
agagcgtat	
gctggccctg	
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gctgtcagcc	
acgaccacga	
cggtacggc	
gcctacagca	
accac	

<210> 8

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Oligonucleotide ZC22162

<400> 8

ccgcggcacc aaccactc

18

<210> 9

<211> 18

<212> DNA
<213> Artificial Sequence

<220>
<223> Oligonucleotide ZC 22168

<400> 9

gtcgcggttc ttcatcag

18